



Draft Genome Sequence of *Streptomyces phaeoluteigriseus* DSM41896

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ABSTRACT The draft genome for the type strain *Streptomyces phaeoluteigriseus* DSM41896 (ISP 5182) is reported. It was classified as a member of the *Streptomyces violaceusniger* clade; however, a polyphasic study showed it was a separate species based on its distinct spore morphology and 16S rRNA sequence. The genome sequence confirms it as a separate species.

The genome of *Streptomyces phaeoluteigriseus* DSM41896 was sequenced. It was originally isolated from soil and incorrectly identified as a member of the *Streptomyces violaceusniger* clade and later described as a separate species based on phenotypic traits and differences in the 16S rRNA sequence (1).

The genomic DNA was extracted from a 3-day culture grown in ISP1 medium (2). The ISOLATE II Genomic DNA kit (Bioline, United Kingdom), including a prelysis lysozyme step, was used for isolation according to the manufacturer's instructions. The library, targeting a 380-bp fragment size, was created using the Next Fast DNA Fragmentation & Library Prep Set for Ion Torrent (New England Biolabs, USA) and an E-Gel system (Invitrogen, USA) for the size selection. The quality assessment of the library was carried out using a dsDNA HS bioanalyzer kit (Agilent, USA).

The draft genome was sequenced using an Ion Torrent PGM at the Strathclyde Institute of Pharmacy and Biomedical Sciences (SIPBS), Glasgow, United Kingdom, using the Hi Q OT2 and Sequencing kit (Life Technologies, Inc., USA). Two runs were performed, one on a 318 chip and one on a 316 Chip v 2 type (Life Technologies, Inc., USA).

The reads were first assembled using SPAdes 3.9 (77 k-mer, single-cell mode, >1,000-bp length) as recommended for high-GC data sets (3). This was used to obtain an 81-gapped contig scaffold using MeDuSa (4), a multidraft-based analysis using 3 related species, *Streptomyces griseus*, *Streptomyces scabiei* and *Streptomyces hygroscopicus*, with full-genome sequences. The total number of contigs in the scaffold is 223, with the largest contig of 306,604 bp and an N_{50} value of 71,307. The total genome size is 8,629,293 bp with a G+C content of 71.5%. The assembly statistics were generated with QUAST 3.2 (5).

The annotation using the RAST server (6, 7) predicted 8,313 coding sequences (CDS), including 74 tRNA genes. The average nucleotide identity (ANI) calculator based on MUMer (8) was utilized and the closest relatives were *Streptomyces griseus* NRRL WC-3645 (86.87%), *Streptomyces stelliscabiei* NRRL B-24447 (86.28%), and *Streptomyces scabiei* 96-08 (86.26%) (9). These results indicate that this strain is a separate species and also support the findings from the polyphasic study of 2007 (1, 10).

The genome was analyzed for secondary metabolite biosynthetic gene clusters using the bioinformatic tool antiSMASH 3.0 (11), and a total of 38 putative secondary metabolite gene clusters were detected, 2 bacteriocins, 2 butyrolactones, 1 ectoine, 1 indole, 1 lantipeptide, 1 lassopeptide, 2 melanin clusters, 10 nonribosomal peptide synthetase (NRPS) clusters (2 type 1 polyketide synthases [t1pks]), 1 nucleoside, 3

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siderophores, 5 terpenes, 2 type 1 polyketides, 3 type 2 polyketides, 1 type 3 polyketide, and 3 other clusters.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [MPOH00000000](#). The version described in this paper is version MPOH02000000.

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